Animal Genetics, 2000, **31**, 420–426

Author Index

Aasland, M, Klungland, H & Lien, S. Two polymorphisms in the bovine mast cell growth factor gene (*MGF*), 345
Aasland, M, Våge, D I, Lien, S & Klungland, H. Resolution of conflicting assignments for the bovine *casein kinase* II??-(*CSNK2A2*) gene, 131
Afanassieff, M *see* Juul-Madsen, H R
Agaba, M *see* Yamakuchi, H
Ahlroth, M K, Kola, E H, Ewald, D, Masabanda, J, Sazanov, A, Fries, R & Kulomaa, M S. Characterization and chromosomal localization of the chicken avidin gene family, 367
Akita, T *see* Wada, Y
Albornoz, J *see* Pérez, T
Aldridge, V *see* Swinburne, J E
Alexander, L J *see* Reed, K M
see also Roberts, M C
Almeida, P A R *see* Diez-Tascón, C
Altet, L *see* Kennedy, L J
Amano, T *see* Omi, T
Andersson, L *see* Edfors-Lilja, I
see also Kijas, J M H
André, C *see* Jouquand, S
Andrews, A E *see* Maddox, J F
Angles, J M *see* Kennedy, L J
Asakawa, S *see* Suzuki, K
Awata, T *see* Wada, Y
Azevedo, M *see* Ferrand, N

Babu, R *see* Sasse, J
Bailey, E, Skow, L, Bernoco, D, DelValle, A, Scavone, M D P, Bowling, A T & Murray, J D. Equine dinucleotide repeat loci *LEX071* through *LEX078*, 286
Barendse, W *see* Gu, Z
see also Tammen, I
Barnes, A *see* Kennedy, L J
Beattie, C W *see* Reed, K M
Beever, J *see* Segers, K
Beh, K J *see* Maddox, J F
Beh, K J, Riffkin, C D, Davies, K P, di Ienno, K L & Maddox, J F. Dinucleotide repeat polymorphism at the ovine *McMA7*, *McMA10*, *McMA13*, *McMA16*, *McMA17*, *McMA27*, *McMA29*, *McMA42*, *McMA47* and *McMA49* loci, 228
Bennett, G L *see* Sonstegard, T S
Berghmans, S *see* Segers, K
Bergknut, N *see* Tammen, I
Bernoco, D *see* Bailey, E
Berryere, T G *see* Schmutz, S M
Beynon, C *see* McConnell, S K J
Bigi, D *see* Davoli, R
Binns, M M *see* Swinburne, J E
Bjørnstad, G, Midthjell, L & Røed, K H. Characterization of ten equine dinucleotide microsatellite loci: *NVHEQ21*, *NVHEQ54*, *NVHEQ67*, *NVHEQ70*, *NVHEQ75*, *NVHEQ77*, *NVHEQ79*, *NVHEQ81*, *NVHEQ82* and *NVHEQ83*, 78
Blažková, P, Kopečný, M, Fontanesi, L, Stratil, A, Davoli, R, Reiner, G & Geldermann, H. Linkage assignments of the porcine *ATP1A2*, *ATP1B1* and *V-ATPase* (*CGI-11*) genes to chromosome 4, 416
Bolla, P *see* Damiani, G
see also Damiani, G
Bonhomme, F *see* Huvet, A
Bosma, A A *see* Davoli, R
Boswell, T *see* Dunn, I C
Bottema, C D K *see* Maddox, J F
Boudry, P *see* Huvet, A
Bowling, A T *see* Bailey, E
see also Caetano, A R
Bowling, A T, Del Valle, A & Bowling, M. A pedigree-based study of mitochondrial D-loop DNA sequence variation among Arabian horses, 1
Bowling, M *see* Bowling, A T
Bozic, P *see* Premzl, M
Bradley, D G *see* Edwards, C J
see also Edwards, C J
Bredbacka, P *see* Koskinen, M T
Breen, M *see* Swinburne, J E
Brem, G *see* Hanslik, S
Brenig, B *see* Dierkes, B
see also Duscher, S
see also Leeb, T
see also Leeb, T
see also Wende, S
Brenneman, R A *see* Wu, X
Broadhead, A *see* Lagziel, A
Brouillette, J A & Venta, P J. *Tth111*I PCR RFLP marker in the canine rod transducin alpha (*GNAT1*) gene, 68
Bruley, C K *see* Smith, J
see also Smith, J
Buchanan, F C *see* Schmutz, S M
Budelli, E *see* Damiani, G
see also Damiani, G
Buitkamp, J, Kollers, S, Durstewitz, G, Fries, R, Welzel, K, Schäfer, K, Kellermann, A & Lehrach, H. Construction and characterization of a gridded cattle BAC library, 347
Bumstead, N *see* Hughes, S
see also Hughes, S
Burke, D *see* Smith, J
Burt, D W *see* Dunn, I C
see also Smith, J
see also Smith, J
Byun, H D *see* Han, S K

Caetano, A R, Murray, J D & Bowling, A T. Polymorphic microsatellites associated with the equine *CKM* and *CMA1* genes, 141
Campbell, E M *see* Fahrenkrug, S C
Campbell, M T *see* Noakes, M A
Cañon, J, Checa, M L, Carleos, C, Vega-Pla, J L, Vallejo, M & Dunner, S. The genetic structure of Spanish Celtic horse breeds inferred from microsatellite data, 39
Carleos, C *see* Cañon, J
Caroli, A *see* Damiani, G
see also Damiani, G
Carter, S D *see* Kennedy, L J
Castellanos, C *see* Óvilo, C
Cepica, S *see* Knoll, A
see also Knoll, A
Cervera, M T *see* Óvilo, C
Charlier, C *see* Segers, K
Checa, M L *see* Cañon, J
Chen, M Y, Huang, S Y, Tsou, H L, Lin, E C, Yang, P C, Kuo, Y H, Huang, T Y & Lee, W C. Polymorphism in the 5′-flanking region of porcine heat shock protein 70.2 gene, 409
Chen, Y *see* Li, K
Chung, H Y *see* Hines, H C
Cockett, N *see* Segers, K
Coimbra, M R M, Hasegawa, O, Kobayashi, K, Koretsugu, S, Naruse, K & Okamoto, N. Four microsatellite markers in the Japanese flounder, *Paralichthys olivaceus*, 72
Coppieters, W *see* Karim, L
Cosenza, G *see* Ramunno, L
Cowan, P J *see* Godwin, J
Craigmile, S *see* Russell, G C
Crawford, A M *see* Diez-Tascón, C
see also Paterson, K A
Cribiu, E P *see* Maddox, J F

d'Apice, A J F *see* Godwin, J
Dalgaard, T S *see* Juul-Madsen, H R
Dall'Olio, S *see* Fontanesi, L
Damiani, G, Florio, S, Budelli, E, Bolla, P & Caroli, A. *Hpa*II PCR-RFLP within a Bov-A2 element in the promoter of the bovine *CYP21* (steroid 21-hydroxylase) gene, 154
Damiani, G, Florio, S, Budelli, E, Bolla, P & Caroli, A. Single nucleotide polymorphisms (SNPs) within Bov-A2 SINE in the second intron of bovine and buffalo k-casein (*CSN3*) gene, 277
Daval, S, Pitel, F, Le Nigen, C, Douaire, M, Vignal, A & Lagarrigue, S. Cloning and mapping of the *ACLY* gene to a chicken microchromosome, 411
Davies, K P *see* Beh, K J
see also Maddox, J F
Davis, G *see* Gu, Z
Davis, M E *see* Hines, H C
Davis, S K *see* Gu, Z
see also Wu, X
Davis, S L F *see* Wu, X

© 2000 International Society for Animal Genetics

Animal Genetics, 2000, **31**, 420–426

Author Index

Aasland, M, Klungland, H & Lien, S. Two polymorphisms in the bovine mast cell growth factor gene (*MGF*), 345
Aasland, M, Våge, D I, Lien, S & Klungland, H. Resolution of conflicting assignments for the bovine *casein kinase* II??-(*CSNK2A2*) gene, 131
Afanassieff, M *see* Juul-Madsen, H R
Agaba, M *see* Yamakuchi, H
Ahlroth, M K, Kola, E H, Ewald, D, Masabanda, J, Sazanov, A, Fries, R & Kulomaa, M S. Characterization and chromosomal localization of the chicken avidin gene family, 367
Akita, T *see* Wada, Y
Albornoz, J *see* Pérez, T
Aldridge, V *see* Swinburne, J E
Alexander, L J *see* Reed, K M
see also Roberts, M C
Almeida, P A R *see* Diez-Tascón, C
Altet, L *see* Kennedy, L J
Amano, T *see* Omi, T
Andersson, L *see* Edfors-Lilja, I
see also Kijas, J M H
André, C *see* Jouquand, S
Andrews, A E *see* Maddox, J F
Angles, J M *see* Kennedy, L J
Asakawa, S *see* Suzuki, K
Awata, T *see* Wada, Y
Azevedo, M *see* Ferrand, N

Babu, R *see* Sasse, J
Bailey, E, Skow, L, Bernoco, D, DelValle, A, Scavone, M D P, Bowling, A T & Murray, J D. Equine dinucleotide repeat loci *LEX071* through *LEX078*, 286
Barendse, W *see* Gu, Z
see also Tammen, I
Barnes, A *see* Kennedy, L J
Beattie, C W *see* Reed, K M
Beever, J *see* Segers, K
Beh, K J *see* Maddox, J F
Beh, K J, Riffkin, C D, Davies, K P, di Ienno, K L & Maddox, J F. Dinucleotide repeat polymorphism at the ovine *McMA7*, *McMA10*, *McMA13*, *McMA16*, *McMA17*, *McMA27*, *McMA29*, *McMA42*, *McMA47* and *McMA49* loci, 228
Bennett, G L *see* Sonstegard, T S
Berghmans, S *see* Segers, K
Bergknut, N *see* Tammen, I
Bernoco, D *see* Bailey, E
Berryere, T G *see* Schmutz, S M
Beynon, C *see* McConnell, S K J
Bigi, D *see* Davoli, R
Binns, M M *see* Swinburne, J E
Bjørnstad, G, Midthjell, L & Røed, K H. Characterization of ten equine dinucleotide microsatellite loci: *NVHEQ21*, *NVHEQ54*, *NVHEQ67*, *NVHEQ70*, *NVHEQ75*, *NVHEQ77*, *NVHEQ79*, *NVHEQ81*, *NVHEQ82* and *NVHEQ83*, 78
Blažková, P, Kopečný, M, Fontanesi, L, Stratil, A, Davoli, R, Reiner, G & Geldermann, H. Linkage assignments of the porcine *ATP1A2*, *ATP1B1* and *V-ATPase* (*CGI-11*) genes to chromosome 4, 416
Bolla, P *see* Damiani, G
see also Damiani, G
Bonhomme, F *see* Huvet, A
Bosma, A A *see* Davoli, R
Boswell, T *see* Dunn, I C
Bottema, C D K *see* Maddox, J F
Boudry, P *see* Huvet, A
Bowling, A T *see* Bailey, E
see also Caetano, A R
Bowling, A T, Del Valle, A & Bowling, M. A pedigree-based study of mitochondrial D-loop DNA sequence variation among Arabian horses, 1
Bowling, M *see* Bowling, A T
Bozic, P *see* Premzl, M
Bradley, D G *see* Edwards, C J
see also Edwards, C J
Bredbacka, P *see* Koskinen, M T
Breen, M *see* Swinburne, J E
Brem, G *see* Hanslik, S
Brenig, B *see* Dierkes, B
see also Duscher, S
see also Leeb, T
see also Leeb, T
see also Wende, S
Brenneman, R A *see* Wu, X
Broadhead, A *see* Lagziel, A
Brouillette, J A & Venta, P J. *Tth111*I PCR RFLP marker in the canine rod transducin alpha (*GNAT1*) gene, 68
Bruley, C K *see* Smith, J
see also Smith, J
Buchanan, F C *see* Schmutz, S M
Budelli, E *see* Damiani, G
see also Damiani, G
Buitkamp, J, Kollers, S, Durstewitz, G, Fries, R, Welzel, K, Schäfer, K, Kellermann, A & Lehrach, H. Construction and characterization of a gridded cattle BAC library, 347
Bumstead, N *see* Hughes, S
see also Hughes, S
Burke, D *see* Smith, J
Burt, D W *see* Dunn, I C
see also Smith, J
see also Smith, J
Byun, H D *see* Han, S K

Caetano, A R, Murray, J D & Bowling, A T. Polymorphic microsatellites associated with the equine *CKM* and *CMA1* genes, 141
Campbell, E M *see* Fahrenkrug, S C
Campbell, M T *see* Noakes, M A
Cañon, J, Checa, M L, Carleos, C, Vega-Pla, J L, Vallejo, M & Dunner, S. The genetic structure of Spanish Celtic horse breeds inferred from microsatellite data, 39
Carleos, C *see* Cañon, J
Caroli, A *see* Damiani, G
see also Damiani, G
Carter, S D *see* Kennedy, L J
Castellanos, C *see* Óvilo, C
Cepica, S *see* Knoll, A
see also Knoll, A
Cervera, M T *see* Óvilo, C
Charlier, C *see* Segers, K
Checa, M L *see* Cañon, J
Chen, M Y, Huang, S Y, Tsou, H L, Lin, E C, Yang, P C, Kuo, Y H, Huang, T Y & Lee, W C. Polymorphism in the 5′-flanking region of porcine heat shock protein 70.2 gene, 409
Chen, Y *see* Li, K
Chung, H Y *see* Hines, H C
Cockett, N *see* Segers, K
Coimbra, M R M, Hasegawa, O, Kobayashi, K, Koretsugu, S, Naruse, K & Okamoto, N. Four microsatellite markers in the Japanese flounder, *Paralichthys olivaceus*, 72
Coppieters, W *see* Karim, L
Cosenza, G *see* Ramunno, L
Cowan, P J *see* Godwin, J
Craigmile, S *see* Russell, G C
Crawford, A M *see* Diez-Tascón, C
see also Paterson, K A
Cribiu, E P *see* Maddox, J F

d'Apice, A J F *see* Godwin, J
Dalgaard, T S *see* Juul-Madsen, H R
Dall'Olio, S *see* Fontanesi, L
Damiani, G, Florio, S, Budelli, E, Bolla, P & Caroli, A. *Hpa*II PCR-RFLP within a Bov-A2 element in the promoter of the bovine *CYP21* (steroid 21-hydroxylase) gene, 154
Damiani, G, Florio, S, Budelli, E, Bolla, P & Caroli, A. Single nucleotide polymorphisms (SNPs) within Bov-A2 SINE in the second intron of bovine and buffalo k-casein (*CSN3*) gene, 277
Daval, S, Pitel, F, Le Nigen, C, Douaire, M, Vignal, A & Lagarrigue, S. Cloning and mapping of the *ACLY* gene to a chicken microchromosome, 411
Davies, K P *see* Beh, K J
see also Maddox, J F
Davis, G *see* Gu, Z
Davis, M E *see* Hines, H C
Davis, S K *see* Gu, Z
see also Wu, X
Davis, S L F *see* Wu, X

© 2000 International Society for Animal Genetics

Davoli, R *see* Blažková, P.
see also Fontanesi, L.
see also Fontanesi, L.
see also Lagziel, A.
Davoli, R, Bigi, D, Fontanesi, L, Zambonelli, P, Yerle, M, Zijlstra, C, Bosma, A A, Robic, A & Russo, V. Mapping of 14 expressed sequence tags (ESTs) from porcine skeletal muscle by somatic cell hybrid analysis, 400
De Luca, J C *see* Giovambattista, G
De Lucia, R F S *see* Rahal, P
Dekomien, G & Epplen, J T. Exclusion of the *PDE6A* gene for generalised progressive retinal atrophy in 11 breeds of dogs, 135
Dekomien, G *see* Runte, M
Del Valle, A *see* Bailey, E
see also Bowling, A T
Delany, M E. Patterns of ribosomal gene variation in elite commercial chicken pure line populations, 110
Delgado, J V *see* Martínez, A M
Delsert, C *see* Huvet, A
DeNise, S *see* Lagziel, A
Dennis, J A *see* Tammen, I
Deppe, A *see* Leeb, T
Derr, J N *see* Schnabel, R D
Dhara, S *see* Lagziel, A
Di Gregorio, P *see* Ramunno, L
Di Ienno, K L *see* Beh, K J
Dierkes, B, Kriegesmann, B, Silva, A, Schneider, M P & Brenig, B. Identification of a *Mae*I RFLP in the insulin-like growth factor-1 (*IGF1*) gene of swamp buffaloes (*Bubalus b. bubalis kerebau*), 70
Diez-Tascón, C, Littlejohn, R P, Almeida, P A R & Crawford, A M. Genetic variation within the Merino sheep breed: analysis of closely related populations using microsatellites, 243
Distl, O *see* Drögemüller, C
Dolf, G *see* Edwards, C J
see also Schelling, C
Dolf, G, Schelling, C, Stahlberger-Saitbekova, N, Fu, B, Schläpfer, J & Yang, F. Seven cosmid-derived canine microsatellites, 410
Domínguez, A *see* Pérez, T
Douaire, M *see* Daval, S
Drögemüller, C & Kempers, A. A *Taq*I PCR-RFLP at the bovine myogenic factor (*MYF5*) gene, 146
Drögemüller, C, Distl, O & Leeb, T. Identification of a highly polymorphic microsatellite within the bovine ectodysplasin A (*ED1*) gene on BTA Xq22-24, 415
Drummond, P *see* Smith, E
Dubrova, Y E *see* Signer, E N
Dulout, F N *see* Giovambattista, G
Dunn, I C, Boswell, T, Friedman-Einat, M, Eshdat, Y, Burt, D W & Paton, I R. Mapping of the leptin receptor gene (*LEPR*) to chicken chromosome 8, 290
Dunn, I *see* Smith, J
Dunner, S *see* Cañon, J
Durstewitz, G *see* Buitkamp, J
Duscher, S, Peters, U & Brenig, B. A polymorphic microsatellite located within the second intron of the Methylmalonyl-CoA Mutase (*MUT*) gene on SSC 1, 339
Dutia, B M *see* Russell, G C
Dvorák, J *see* Knoll, A
see also Knoll, A
Dzapo, V *see* Reiner, G

Edfors-Lilja, I, Wattrang, E, Andersson, L & Fossum, C. Mapping quantitative trait loci for stress induced alterations in porcine leukocyte numbers and functions, 186
Edwards, C J, Dolf, G, Looft, C, Loftus, R T & Bradley, D G. Relationships between the endangered Pustertaler-Sprinzen and three related European cattle breeds as analysed with 20 microsatellite loci, 329
Edwards, C J, Gaillard, C, Bradley, D G & MacHugh, D E. Y-specific microsatellite polymorphisms in a range of bovid species, 127
Eggen, A *see* Gautier, M
Eler, J P *see* Rahal, P
Ellendorff, F *see* Klein, S
Elo, K *see* Gu, Z
Epplen, J T *see* Dekomien, G
see also Runte, M
Erhardt, G *see* Gu, Z
Escayg, A P *see* Hickford, J G H
Eshdat, Y *see* Dunn, I C
Everts, R E *see* Versteeg, S A
Everts, R E, Rothuizen, J & Van Oost, B A. Identification of a premature stop codon in the melanocyte-stimulating hormone receptor gene (*MC1R*) in Labrador and Golden retrievers with yellow coat colour, 194
Ewald, D *see* Ahlroth, M K

Fahrenkrug, S C, Campbell, E M, Vallet, J L & Rohrer, G A. Physical assignment of the porcine erythropoietin receptor gene to SSC2, 69
Fan, B *see* Li, K
Ferrand, N, Azevedo, M & Mougel, F. A diallelic short tandem repeat $(CCCCG)_{4 \text{ or } 5}$, located in intron 1 of rabbit α-globin gene, 74
Ferraz, J B S *see* Rahal, P
Florio, S *see* Damiani, G
see also Damiani, G
Fontanesi, L *see* Blažková, P
see also Davoli, R
Fontanesi, L, Davoli, R, Dall'olio, S & Russo, V. Linkage assignment of the fast skeletal alkali myosin light polypeptide 1 (*MYL1*) gene to porcine chromosome 15, 414
Fontanesi, L, Davoli, R, Milc, J & Russo, V. Linkage mapping of the ?-B-crystallin (*CRYAB*) gene to porcine chromosome 9, 287
Ford, J J *see* Li, M D
Fossum, C *see* Edfors-Lilja, I
Foster, J *see* Smith, E
Francino, O *see* Kennedy, L J
Fraser, D C *see* Russell, G C
Friedman-Einat, M *see* Dunn, I C
Fries, R *see* Ahlroth, M K
see also Buitkamp, J
see also Kollers, S
see also Smith, J
Fu, B *see* Dolf, G
Fujishima, N *see* Suzuki, K
Fürbass, R *see* Vanselow, J
Furukawa, T *see* Wada, Y

Gäfvert, S *see* Kijas, J M H
Gaillard, C *see* Edwards, C J
see also Ritz, L R
Galibert, F *see* Jeoung, D
see also Jouquand, S
Gallagher Jr, D S *see* Wu, X
Gallo, D *see* Ramunno, L
Gamulin, V *see* Premzl, M
Garcia, J F *see* Rahal, P
Garrett, W M *see* Sonstegard, T S
Gasbarre, L C *see* Sonstegard, T S
Gattermann, R *see* Maak, S
Gautier, M, Laurent, P & Eggen, A. Syntenic assignment of the selectin P gene (*SELP*) to bovine chromosome 16, 343
Geldermann, H *see* Blažková, P
see also Knoll, A
see also Reiner, G
see also Stratil, A
Gellin, J *see* Pitel, F
Georges, M *see* Karim, L
see also Segers, K
Gerlach, J A *see* Kennedy, L J
Gill, C A *see* Maddox, J F
Giovambattista, G, Ripoli, M V, De Luca, J C, Mirol, P M, Lirón, J P & Dulout, F N. Male-mediated introgression of *Bos indicus* genes into Argentine and Bolivian Creole cattle breeds, 302
Glass, E J *see* Russell, G C
Glazko, V *see* Lagziel, A
Glowatzki-Mullis, M-L *see* Ritz, L R
Godwin, J, Lee, J H, Cowan, P J, d'Apice, A J F & Moran, C. *ICAM2* maps to porcine chromosome 12, 404
Gomez-Raya, L *see* Gu, Z
Gray, I S & Yuzbasiyan-Gurkan, V. A single nucleotide (T–G) polymorphism within intron 23 of the canine *BRCA1* gene, 76
Grobet, L *see* Karim, L
Grosse, W M, Kappes, S M & McGraw, R A. Linkage mapping and comparative analysis of bovine expressed sequence tags (ESTs), 171
Grosse, W M, Kossarek, L M, Kappes, S M & McGraw, R A. Two bovine dinucleotide repeat polymorphisms: *RM084* and *RM171*, 73
Grosz, M *see* Gu, Z
Gu, Z, Gomez-Raya, L, Våge, D I, Elo, K, Barendse, W, Davis, G, Grosz, M, Erhardt, G, Kalm, E, Reinsch, N, Kappes, S M, Stone, R T, Davis, S K, Taylor, J F & Kirkpatrick, B W. Consensus and comprehensive linkage maps of bovine chromosome 7, 206

Ha, J *see* Jeoung, D
Haegeman, A, Van Zeveren, A & Peelman, L J. New mutation in exon 2 of the bovine leptin gene, 79
Hamilton, R *see* Smith, E
Han, S K, Shin, Y C & Byun, H D. Biochemical, molecular and physiological characterization of a new ?-casein variant detected in Korean Cattle, 49
Hanotte, O *see* Jianlin, H
see also Lagziel, A
see also Schmidt, P
Hanslik, S, Harr, B, Brem, G & Schlötterer, C. Microsatellite analysis reveals substantial genetic differentiation between contemporary New World and Old World Holstein Friesian populaitons, 31
Happ, G M *see* Kennedy, L J
Hara, K *see* Kobayashi, N
see also Yamakuchi, H
Hardge, T *see* Wimmers, K
Harr, B *see* Hanslik, S
Hasegawa, O *see* Coimbra, M R M
see also Tozaki, T
see also Tozaki, T
Henry, H M *see* Jenkins, Z A
Hickford, J G H, Ridgway, H J & Escayg, A P. Evolution of the ovine MHC *DQA* region, 200
Hines, H C, Chung, H Y & Davis, M E. Genetic variations in the ovine calpain regulatory subunit, 140
Hiraiwa, H *see* Suzuki, K
Hirano, T *see* Kobayashi, N
see also Yamakuchi, H
Hirota, K *see* Kakoi, H
see also Tozaki, T
see also Tozaki, T
Hitte, C *see* Jeoung, D
see also Jouquand, S
Hořín, P & Matiasovic, J. Two polymorphic markers for the horse *SLC11A1* (*NRAMP1*) gene, 152
Horst, P *see* Wimmers, K
Huang, S Y *see* Chen, M Y
Huang, T Y *see* Chen, M Y
Hughes, S & Bumstead, N. The gene encoding a chicken chemokine with homology to human *SCYC1* maps to chromsome 1, 142
Hughes, S & Bumstead, N. The gene encoding the chicken chemokine K60 maps to chromosome 4, 417
Huvet, A, Boudry, P, Ohresser, M, Delsert, C & Bonhomme, F. Variable microsatellites in the Pacific Oyster *Crassostrea gigas* and other cupped oyster species, 71

Ide, H *see* Kunieda, T
Iida, M *see* Suzuki, K
Imakawa, K *see* Kobayashi, N
Inage, Y *see* Wada, Y
Ishida, N *see* Tozaki, T
see also Tozaki, T
Ishii, K *see* Wada, Y
Ito, Y *see* Wada, Y
Itoh, T *see* Kobayashi, N
see also Sugai, N
Iwamoto, S *see* Omi, T

Jeanplong, F, Sharma, M, Paterson, K A, Morris, C A & Kambadur, R. Polymorphism in dinucleotide repeat (BTAFJ1) upstream to the bovine myostatin locus, 340
Jeffreys, A J *see* Signer, E N
Jenkins, Z A, Henry, H M, Sise, J A & Montgomery, G W. Follistatin (FST), growth hormone receptor (GHR) and prolactin receptor (PRLR) genes map to the same region of sheep chromosome 16, 280
Jenneckens, I *see* Ludwig, A
Jeoung, D, Myeong, H, Lee, H, Ha, J, Galibert, F, Hitte, C & Park, C. A SINE element in the canine D2 dopamine receptor gene and its chromosomal location, 334
Jianlin, H, Mburu, D, Ochieng, J, Kaufmann, B, Rege, J E O & Hanotte, O. Application of New World Camelidae microsatellite primers for amplification of polymorphic loci in Old World camelids, 405
Johnson, J S *see* Rexroad III, C E
Jónasdóttir, T J, Mellersh, C S, Moe, L, Vignaux, F, Ostrander, E A & Lingaas, F. Chromosomal assignment of canine *TSC2*, *PKD1* and *CLN3* genes by radiation hybrid- and linkage analyses, 123
Jones, C T *see* Smith, J
Jouquand, S, Priat, C, Hitte, C, Lachaume, P, André, C & Galibert, F. Identification and characterization of a set of 100 tri- and dinucleotide microsatellites in the canine genome, 266
Juneja, R K *see* Kijas, J M H
Juul-Madsen, H R, Dalgaard, T S & Afanassieff, M. Molecular characterization of major and minor *MHC* class I and II genes in B^{21}-like haplotypes in chickens, 252

Kajii, E *see* Omi, T
Kakoi, H *see* Tozaki, T
see also Tozaki, T
Kakoi, H, Tozaki, T, Hirota, K, Mashima, S, Kurosawa, M & Miura, N. Ten equine microsatellite loci: *TKY25*, *TKY26*, *TKY27*, *TKY28*, *TKY29*, *TKY267*, *TKY268*, *TKY269*, *TKY270* and *TKY271*, 68
Kalm, E *see* Gu, Z
Kambadur, R *see* Jeanplong, F
Kang, N *see* Maddox, J F
Kang'a, S *see* Schmidt, P
Kappes, S M *see* Grosse, W M
see also Grosse, W M
see also Gu, Z
see also Sonstegard, T S
Karim, L, Coppieters, W, Grobet, L, Valentini, A & Georges, M. Convenient genotyping of six myostatin mutations causing double-muscling in cattle using a multiplex oligonucleotide ligation assay, 396
Kaufmann, B *see* Jianlin, H
Kellermann, A *see* Buitkamp, J
Kempers, A *see* Drögemüller, C
Kennedy, L J, Altet, L, Angles, J M, Barnes, A, Carter, S D, Francino, O, Gerlach, J A, Happ, G M, Ollier, W E R, Polvi, A, Thomson, W & Wagner, J L. Nomenclature for factors of the Dog Major Histocompatibility System (DLA), 1998: first report of the ISAG DLA Nomenclature Committee, 52
Khoo, S K, Ozaki, A, Sakamoto, T & Okamoto, N. Four highly polymorphic dinucleotide microsatellites in rainbow trout (*Oncorhynchus mykiss*), 73
Kijas, J M H, Juneja, R K, Gäfvert, S & Andersson, L. Detection of the causal mutation for canine leukocyte adhesion deficiency (CLAD) using pyrosequencing, 326
Kim, K S, Marklund, S & Rothschild, M F. The porcine melanocortin-5 receptor (*MC5R*) gene: polymorphisms, linkage and physical mapping, 230
Kinne, J *see* Sasse, J
Kirkpatrick, B W *see* Gu, Z
Kittleson, M D *see* Magnon, A L
see also Magnon, A L
see also Meurs, K M
Klein, S & Ellendorff, F. Localisation of *Xho1* repetitive sequences on autosomes in addition to the W
chromosome in chickens and its relevance for sex diagnosis, 104
Klungland, H *see* Aasland, M
see also Aasland, M
see also Olsen, H G
Knoll, A *see* Stratil, A
Knoll, A, Putnová, L, Dvořák, J & Čepica, S. A *Nci*I PCR-RFLP within intron 2 of the porcine insulin-like growth factor (*IGF2*) gene, 150
Knoll, A, Putnová, L, Dvořák, J, Rohrer, G A & Čepica, S. Linkage mapping of an *Ava*I PCR-RFLP within the porcine uncoupling protein 3 (*UCP3*) gene, 156
Knoll, A, Stratil, A, Moser, G & Geldermann, H. Characterization of three PCR-RFLPs in an intron of the porcine liver- and red cell-type pyruvate kinase (*PKLR*) gene, 234
Kobayashi, E *see* Wada, Y
Kobayashi, K *see* Coimbra, M R M
Kobayashi, N, Hirano, T, Maruyama, S, Matsuno, H, Mukoujima, K, Morimoto, H, Noike, H, Tomimatsu, H, Hara, K, Itoh, T, Imakawa, K, Nakayama, H, Nakamaru, T & Sugimoto, Y. Genetic mapping of a locus associated with bovine chronic interstitial nephritis to chromosome 1, 91
Kohek, M B F *see* Rahal, P
Kola, E H *see* Ahlroth, M K
Kollers, S & Fries, R. Physical mapping of the interleukin-7 receptor gene (*IL7R*) to bovine chromosome 20q15-q17, 290
Kollers, S *see* Buitkamp, J
Konfortov, B *see* Kunieda, T
Kopečný, M *see* Blažková, P
Kopecný, M *see* Stratil, A
Koretsugu, S *see* Coimbra, M R M

Koskinen, M T & Bredbacka, P. Assessment of the population structure of five Finnish dog breeds with microsatellites, 310
Kossarek, L M *see* Grosse, W M
Krempler, A *see* Wende, S
Kriegesmann, B *see* Dierkes, B
see also Leeb, T
Kubícková, S *see* Musilová, P
Kubota, C *see* Yamakuchi, H
Kühn, C *see* Vanselow, J
Kühn, Ch *see* Schmidt, P
Kulomaa, M S *see* Ahlroth, M K
Kunieda, T, Ide, H, Nakagiri, M, Yoneda, K, Konfortov, B & Ogawa, H. Localization of the locus responsible for Chediak-Higashi syndrome in cattle to bovine chromosome 28, 87
Kuo, Y H *see* Chen, M Y
Kurosawa, M *see* Kakoi, H
Kusumoto, H *see* Wada, Y

Lachaume, P *see* Jouquand, S
Lagarrigue, S *see* Daval, S
Lagziel, A, DeNise, S, Hanotte, O, Dhara, S, Glazko, V, Broadhead, A, Davoli, R, Russo, V & Soller, M. Geographic and breed distribution of an *Msp* I PCR-RFLP in the bovine growth hormone (bGH) gene, 210
Langner, Ch *see* Schmidt, P
Larsson, U *see* Tammen, I
Latronico, A C *see* Rahal, P
Laurent, P *see* Gautier, M
Law, A S *see* Smith, J
Le Nigen, C *see* Daval, S
Leamon, J *see* McConnell, S K J
Lee, H *see* Jeoung, D
Lee, J H *see* Godwin, J
Lee, W C *see* Chen, M Y
Leeb, T *see* Drögemüller, C
Leeb, T, Deppe, A, Kriegesmann, B & Brenig, B. Genomic structure and nucleotide polymorphisms of the porcine agouti signalling protein gene (*ASIP*), 335
Leeb, T, Pfeiffer, I & Brenig, B. Two highly polymorphic microsatellites between the canine *DAG1* and *BSN* genes on CFA20q15.1-15.2, 337
Lehrach, H *see* Buitkamp, J
Lewis, A M *see* Smith, J A
Li, K, Chen, Y, Moran, C, Fan, B, Zhao, S & Peng, Z. Analysis of diversity and genetic relationships between four Chinese indigenous pig breeds and one Australia commercial pig breed, 322
Li, M D, Rohrer, G A, Wise, T H & Ford, J J. Identification and characterization of a new allele for the beta subunit of follicle-stimulating hormone in Chinese pig breeds, 28
Lien, S *see* Aasland, M
see also Aasland, M
see also Olsen, H G
Lin, E C *see* Chen, M Y
Lindgren, G. Ten equine dinucleotide microsatellite repeats *HTG18-19*, *HTG22-24*, *HTG26-27*, *HGT29-30* and *HTG32*, 145
Lingaas, F *see* Jónasdóttir, T J
Lirón, J P *see* Giovambattista, G
Littlejohn, R P *see* Diez-Tascón, C
Lockhart, L *see* Swinburne, J E
Loftus, R T *see* Edwards, C J
Looft, C *see* Edwards, C J
Ludwig, A & Jenneckens, I. A PCR test for mitochondrial heteroplasmy in sturgeon, 153

Maak, S, Neumann, K, Von Lengerken, G & Gattermann, R. First seven microsatellites developed for the Peking duck (*Anas platyrhynchos*), 233
MacHugh, D E *see* Edwards, C J
see also Ritz, L R
Maclean, I *see* Wiener, P
Maddox, J F *see* Beh, K J
Maddox, J F, Andrews, A E, Gill, C A & Bottema, C D K. Linkage and physical mapping of the sheep perforin (*PRF1*) gene to OAR 25, 231
Maddox, J F, Riffkin, C D & Beh, K J. Dinucleotide repeat polymorphism at the ovine *McMA1*, *McMA2*, *McMA5*, *McMA8*, *McMA9*, *McMA11*, *McMA14*, *McMA20*, *McMA24* and *McMA26* loci, 148
Maddox, J F, Schibler, L, Cribiu, E P, Kang, N, Davies, K P & Vaiman, D. Linkage mapping of goat ChirUCO, LSCV and SR-CRSP microsatellites in sheep, 145
Maddox, J F. Chromosomal assignments and polymorphism information content in sheep for 12 cattle microsatellites, 144
Magnon, A L, Meurs, K M, Kittleson, M D & Ware, W A. A highly polymorphic marker identified in intron 15 of the feline cardiac troponin T gene by SSCP analysis, 236
Magnon, A L, Meurs, K M, Kittleson, M D & Ware, W A. Single nucleotide polymorphisms in intron 5 of the feline myosin regulatory light chain gene detected by SSCP analysis, 281
Mariasegaram, M *see* Sasse, J
Marklund, S *see* Kim, K S
Marklund, S, Tuggle, C K & Rothschild, M F. Mapping of the *CYP1A1*, *SSTR1* and *TTF1* genes to pig chromosome 7q refines the porcine–human comparative map, 318
Marti, E *see* Swinburne, J E
Martínez, A M, Delgado, J V, Rodero, A & Vega-Pla, J L. Genetic structure of the Iberian pig using microsatellities, 295
Martínez-Zapater, J M *see* Óvilo, C
Maruyama, S *see* Kobayashi, N
Masabanda, J *see* Ahlroth, M K
see also Smith, J
Mashima, S *see* Kakoi, H
see also Tozaki, T
see also Tozaki, T
Masina, P *see* Ramunno, L
Mathur, P K *see* Wimmers, K
Matiasovic, J *see* Hořín, P
Matsumoto, T *see* Wada, Y
Matsuno, H *see* Kobayashi, N
Mburu, D *see* Jianlin, H
McConnell, S K J, Beynon, C, Leamon, J & Skibinski, D O F. Microsatellite marker based genetic linkage maps of *Oreochromis aureus* and *O. niloticus* (Cichlidae): extensive linkage group segment homologies revealed., 214
McCracken, J Y *see* Molenaar, A
McGraw, R A *see* Grosse, W M
see also Grosse, W M
Mellersh, C S *see* Jónasdóttir, T J
Meurs, K M *see* Magnon, A L
see also Magnon, A L
Meurs, K M, Kittleson, M, Spangler, E, Ware, W A, Womack, J E & Towbin, J A. Nine polymorphisms within the head and hinge region of the feline cardiac ?-myosin heavy chain gene, 231
Meyer, A *see* Noack, K
Meyers, S *see* Segers, K
Mickelson, J R *see* Roberts, M C
Midthjell, L *see* Bjørnstad, G
Mikawa, S *see* Sugai, N
see also Wada, Y
Milazzotto, M P *see* Rahal, P
Milc, J *see* Fontanesi, L
Mirol, P M *see* Giovambattista, G
Miura, N *see* Kakoi, H
see also Tozaki, T
see also Tozaki, T
see also Tozaki, T
Miyake, M *see* Wada, Y
Mizoshita, K *see* Yamakuchi, H
Moe, L *see* Jónasdóttir, T J
Molenaar, A, Wheeler, T T, McCracken, J Y & Seyfert, H-M. The *STAT3*-encoding gene resides within the 40 kbp gap between the *STAT5A*- and *STAT5B*-encoding genes in cattle, 339
Monbrun, C *see* Pitel, F
Montgomery, G W *see* Jenkins, Z A
Moore, S S *see* Whan, V A
Moran, C *see* Godwin, J
see also Li, K
see also Tammen, I
Morimoto, H *see* Kobayashi, N
Morrice, D R *see* Smith, J
Morris, C A *see* Jeanplong, F
Moser, G *see* Knoll, A
see also Stratil, A
Mougel, F *see* Ferrand, N
Mukoujima, K *see* Kobayashi, N
Murakami, Y *see* Suzuki, K
Murase, A *see* Wada, Y
Murray, J D *see* Bailey, E
see also Caetano, A R
Murtaugh, J *see* Reed, K M
see also Roberts, M C

Musilová, P, Kubícková, S, Vozdová, M & Rubes, J. Mapping of the oncogene c-myc (*MYC*) and the breast cancer susceptibility gene (*BRCA2*) in the pig by FISH, 154
Myeong, H *see* Jeoung, D

Nahashon, S *see* Smith, E
Nakagiri, M *see* Kunieda, T
Nakamaru, T *see* Kobayashi, N
Nakayama, H *see* Kobayashi, N
Naruse, K *see* Coimbra, M R M
Neumann, K *see* Maak, S
Nielsen, V H & Thomsen, B. Genetic assignment of the *GLI* gene to porcine chromosome 5, 408
Nishimura, K *see* Oishi, M
Noack, K, Wilson, A B & Meyer, A. Broad taxonomic applicability of microsatellites developed for the highly polymorphic neotropical cichlid, *Amphilophus citrinellum*, 151
Noakes, M A, Campbell, M T & Van Hest, B J. The chicken *CLOCK* gene maps to chromosome 4, 333
Noike, H *see* Kobayashi, N

Ochieng, J *see* Jianlin, H
Ogawa, H *see* Kunieda, T
Ohresser, M *see* Huvet, A
Oishi, M, Taniguchi, Y, Nishimura, K, Yamada, T & Sasaki, Y. Characterisation of gene expression in bovine adipose tissue before and after fattening, 166
Okamoto, N *see* Coimbra, M R M
see also Khoo, S K
Oliver, R A *see* Russell, G C
Ollier, W E R *see* Kennedy, L J
Olsen, H G, Våge, D I, Lien, S & Klungland, H. A DNA polymorphism in the bovine *c-kit* gene, 71
Omi, T, Tsuchida, S, Onishi, A, Amano, T, Tanaka, K, Iwamoto, S & Kajii, E. Molecular basis of esterase D polymorphism in the pig, 412
Onishi, A *see* Omi, T
Ostrander, E A *see* Jónasdóttir, T J
Óvilo, C, Cervera, M T, Castellanos, C & Martínez-Zapater, J M. Characterisatin of Iberian pig genotypes using AFLP markers, 117
Owens, E K *see* Rexroad III, C E
Ozaki, A *see* Khoo, S K

Pappalardo, M *see* Ramunno, L
Park, C *see* Jeoung, D
Pastore, N *see* Ramunno, L
Paterson, K A & Crawford, A M. Ovine microsatellite *OarKP6* isolated from a BAC containing the ovine interferon gamma gene, 343
Paterson, K A *see* Jeanplong, F
Paton, I R *see* Dunn, I C
see also Smith, J
see also Smith, J
Peelman, L J *see* Haegeman, A
Peng, Z *see* Li, K
Pérez, T, Albornoz, J & Domínguez, A. A panel of bovine and caprine microsatellites suitable as markers in chamois, 344
Peters, U *see* Duscher, S
Pfeiffer, I *see* Leeb, T
Pitel, F *see* Daval, S
Pitel, F, Monbrun, C, Gellin, J & Vignal, A. The chicken LEP (OB) gene has not been mapped, 281
Polvi, A *see* Kennedy, L J
Ponce de Leon, F A *see* Smith, J
Ponsuksili, S *see* Trakooljul, N
see also Wimmers, K
Powell, E *see* Smith, E
Premzl, M, Bozic, P & Gamulin, V. *PRNP* octarepeat allele genotype frequencies among the modern and rare cattle breeds in Croatia, 407
Priat, C *see* Jouquand, S
Putnová, L *see* Knoll, A
see also Knoll, A

Rahal, P, Latronico, A C, Kohek, M B F, de Lucia, R F S, Milazzotto, M P, Wheeler, M B, Ferraz, J B S, Eler, J P & Garcia, J F. Polymorphisms in the bovine follicle-stimulating hormone receptor gene, 280
Ramlal, S *see* Smith, E
Ramunno, L, Cosenza, G, Pappalardo, M, Pastore, N, Gallo, D, Di Gregorio, P & Masina, P. Identification of the goat *CSN1S1*^{F} allele by means of PCR-RFLP method, 342
Reed, K M, Roberts, M C, Murtaugh, J, Beattie, C W & Alexander, L J. Eight new dinucleotide microsatellite loci in turkey (*Meleagris gallopavo*), 140
Rege, J E O *see* Jianlin, H
Reiner, G *see* Blažková, P
Reiner, G, Willems, H, Geldermann, H & Dzapo, V. Four PCR-RFLPs and a sequence polymorphism in the porcine c-myc proto-oncogene and confirmation of the chromosomal localisation on SSC4 by linkage mapping, 155
Reinsch, N *see* Gu, Z
Reissmann, M *see* Wagner, H-J
Rexroad III, C E, Owens, E K, Johnson, J S & Womack, J E. A 12 000 rad whole genome radiation hybrid panel for high resolution mapping in cattle: characterization of the centromeric end of chromsome 1, 262
Ridgway, H J *see* Hickford, J G H
Riffkin, C D *see* Beh, K J
see also Maddox, J F
Ripoli, M V *see* Giovambattista, G
Ritz, L R, Glowatzki-Mullis, M-L, Machugh, D E & Gaillard, C. Phylogenetic analysis of the tribe Bovini using microsatellites, 178
Roberts, M C *see* Reed, K M
Roberts, M C, Murtaugh, J, Valberg, S J, Mickelson, J R & Alexander, L J. Twenty-one new equine dinucleotide repeat microsatellites, 141
Robic, A *see* Davoli, R
Rodero, A *see* Martínez, A M
Rodriguez, L *see* Smith, E
Røed, K H *see* Bjørnstad, G
Rohrer, G A *see* Fahrenkrug, S C
see also Knoll, A
see also Li, M D
Rothschild, M F *see* Kim, K S
see also Marklund, S
Rothuizen, J *see* Everts, R E
Rubes, J *see* Musilová, P
Runte, M, Dekomien, G & Epplen, J T. Evaluation of *RDS/Peripherin* and *ROM1* as candidate genes in generalised progressive retinal atrophy and exclusion of digenic inheritance, 223
Russell, G C, Fraser, D C, Craigmile, S, Oliver, R A, Dutia, B M & Glass, E J. Sequence and transfection of *BoLA-DRB3* cDNAs, 219
Russo, V *see* Davoli, R
see also Fontanesi, L
see also Fontanesi, L
see also Lagziel, A

Sakamoto, T *see* Khoo, S K
Sasaki, Y *see* Oishi, M
Sasse, J, Mariasegaram, M, Babu, R, Kinne, J & Wernery, U. South American camelid microsatellite amplification in *Camelus dromedarius*, 75
Sawazaki, T *see* Sugai, N
Sazanov, A *see* Ahlroth, M K
see also Smith, J
Scavone, M D P *see* Bailey, E
Schäfer, K *see* Buitkamp, J
Schellander, K *see* Trakooljul, N
Schelling, C *see* Dolf, G
Schelling, C, Schläpfer, J, Vennos, C, Stahlberger-Saitbekova, N & Dolf, G. Seven novel cosmid-derived canine microsatellites, 77
Schibler, L *see* Maddox, J F
Schläpfer, J *see* Dolf, G
see also Schelling, C
Schlötterer, C *see* Hanslik, S
Schmidt, P, Kühn, Ch, Kang'a, S, Hanotte, O, Vanselow, J, Anton, I, Langner, Ch & Schwerin, M. Interleukin-12 p35 encoding gene of cattle and sheep harbours a polymorphic T stretch in intron 4, 283
Schmutz, S M, Berryere, T G & Buchanan, F C. An SNP in *DCT* is used for linkage mapping on cattle chromosome 12, 336
Schnabel, R D, Ward, T J & Derr, J N. Validation of 15 icrosatellites for parentage testing in North American bison, *Bison bison* and domestic cattle, 360
Schneider, M P *see* Dierkes, B
Schwerin, M *see* Schmidt, P
see also Vanselow, J
Segers, K, Vaiman, D, Berghmans, S, Shay, T, Meyers, S, Beever, J, Cockett, N, Georges, M & Charlier, C. Construction and characterization of an ovine BAC contig spanning the callipyge locus, 352
Seyfert, H-M *see* Molenaar, A
Sharma, M *see* Jeanplong, F
Shay, T *see* Segers, K
Shi, L *see* Smith, E

Shimanuki, S *see* Suzuki, K
see also Wada, Y
Shimizu, N *see* Suzuki, K
Shin, Y C *see* Han, S K
Signer, E N, Dubrova, Y E & Jeffreys, A J. Are DNA profiles breed-specific? A pilot study in pigs, 273
Silva, A *see* Dierkes, B
Sise, J A *see* Jenkins, Z A
Skibinski, D O F *see* McConnell, S K J
Skow, L *see* Bailey, E
Slappendel, R J *see* Versteeg, S A
Smith, E, Shi, L, Drummond, P, Rodriguez, L, Hamilton, R, Powell, E, Nahashon, S, Ramlal, S, Smith, G & Foster, J. Development and characterization of expressed sequence tags for the turkey (*Meleagris gallopavo*) genome and comparative sequence analysis with other birds, 62
Smith, G *see* Smith, E
Smith, J A, Lewis, A M, Wiener, P & Williams, J L. Genetic variation in the bovine myostatin gene in UK beef cattle: Allele frequencies and haplotype analysis in south Devon, 306
Smith, J, Bruley, C K, Paton, I R, Dunn, I, Jones, C T, Windsor, D, Morrice, D R, Law, A S, Masabanda, J, Sazanov, A, Waddington, D, Fries, R & Burt, D W. Differences in gene density on chicken macrochromosomes and microchromosomes, 96
Smith, J, Paton, I R, Bruley, C K, Windsor, D, Burke, D, Ponce de Leon, F A & Burt, D W. Integration of the genetic and physical maps of the chicken macrochromosomes, 20
Soller, M *see* Lagziel, A
Song, Y *see* Wu, X
Sonstegard, T S, Garrett, W M, Bennett, G L, Kappes, S M, Zarlenga, D S & Gasbarre, L C. Mapping of seven bovine cytokine genes involved in T-lymphocyte growth, differentiation and immune response, 406
Spangler, E *see* Meurs, K M
Stahlberger-Saitbekova, N *see* Dolf, G
see also Schelling, C
Stone, R T *see* Gu, Z
Stratil, A *see* Blažková, P
see also Knoll, A
Stratil, A, Knoll, A, Moser, G, Kopečný, M & Geldermann, H. The porcine adenosine monophosphate deaminase 1 (*AMPD1*) gene maps to chromosome 4, 147
Sugai, N *see* Wada, Y
Sugai, N, Sawazaki, T, Itoh, T, Mikawa, S, Wada, Y & Yasue, H. Physical assignment of markers, *SJ017*, *SJ042*, and *SJ065* to swine chromosome X, 240
Sugimoto, Y *see* Kobayashi, N
see also Yamakuchi, H
Sugiyama, T *see* Wada, Y
Suzuki, K, Asakawa, S, Iida, M, Shimanuki, S, Fujishima, N, Hiraiwa, H, Murakami, Y, Shimizu, N & Yasue, H. Construction and evaluation of a porcine bacterial artificial chromosome library, 8
Swinburne, J E, Lockhart, L, Aldridge, V, Marti, E, Breen, M & Binns, M M. Characterisation of 25 new physically mapped horse microsatellite loci: *AHT24-48*, 237

Tabara, N *see* Yamakuchi, H
Tammen, I, Larsson, U, Bergknut, N, Barendse, W, Moran, C & Dennis, J A. Physical and linkage mapping of the bovine acidic ?-glucosidase gene to chromosome 19, 285
Tanaka, K *see* Omi, T
Taniguchi, Y *see* Oishi, M
Taylor, J F *see* Gu, Z
see also Wu, X
Thomsen, B *see* Nielsen, V H
Thomson, W *see* Kennedy, L J
Todoroki, J *see* Yamakuchi, H
Tomimatsu, H *see* Kobayashi, N
Tomita, M *see* Tozaki, T
see also Tozaki, T
see also Tozaki, T
Towbin, J A *see* Meurs, K M
Tozaki, T *see* Kakoi, H
Tozaki, T, Kakoi, H, Mashima, S, Hirota, K, Hasegawa, T, Ishida, N, Miura, N & Tomita, M. The isolation and characterization of 18 equine microsatellite loci, *TKY272–TKY289*, 149
Tozaki, T, Kakoi, H, Mashima, S, Hirota, K, Hasegawa, T, Ishida, N, Miura, N & Tomita, M. The isolation and characterization of 34 equine microsatellite loci, *TKY290-TKY323*, 234
Tozaki, T, Mashima, S, Miura, N & Tomita, M. The equine *CD74* gene has a polymorphic $(CAG)_n$ repeat in the 5′-untranslated region, 239
Trakooljul, N, Ponsuksili, S, Schellander, K & Wimmers, K. A highly polymorphic repetitive polypyrimidine polypurine (CCTTT)n sequence in the 5′untranslated sequence of the porcine androgen receptor gene, 288
Tsou, H L *see* Chen, M Y
Tsuchida, S *see* Omi, T
Tuggle, C K *see* Marklund, S

Uchida, Y *see* Wada, Y

Våge, D I *see* Aasland, M
see also Gu, Z
see also Olsen, H G
Vaiman, D *see* Maddox, J F
see also Segers, K
Valberg, S J *see* Roberts, M C
Valentini, A *see* Karim, L
Vallejo, M *see* Cañon, J
Vallet, J L *see* Fahrenkrug, S C
Valle-Zarate, A *see* Wimmers, K
Van Hest, B J *see* Noakes, M A
Van Oost, B A *see* Everts, R E
see also Versteeg, S A
Van Zeveren, A *see* Haegeman, A
Vanselow, J *see* Schmidt, P
Vanselow, J, Kühn, C, Fürbass, R & Schwerin, M. Isolation of the bovine *CYP19* promoter 1.2 and identification of genetic variants, 337
Vega-Pla, J L *see* Cañon, J
see also Martínez, A M
Vennos, C *see* Schelling, C
Venta, P J *see* Brouillette, J A
Versteeg, S A, Everts, R E, Slappendel, R J & Van Oost, B A. Genetic and physical ordering of polymorphic DNA markers in the region of the canine von Willebrand factor gene, 413
Vignal, A *see* Daval, S
see also Pitel, F
Vignaux, F *see* Jónasdóttir, T J
Von Lengerken, G *see* Maak, S
Vozdová, M *see* Musilová, P

Wada, Y *see* Sugai, N
Wada, Y, Akita, T, Awata, T, Furukawa, T, Sugai, N, Inage, Y, Ishii, K, Ito, Y, Kobayashi, E, Kusumoto, H, Matsumoto, T, Mikawa, S, Miyake, M, Murase, A, Shimanuki, S, Sugiyama, T, Uchida, Y, Yanai, S & Yasue, H. Quantitative trait loci (QTL) analysis in a Meishan × Göttingen cross population, 376
Waddington, D *see* Smith, J
Wagner, H-J & Reissmann, M. New polymorphism detected in the horse *MC1R* gene, 289
Wagner, J L *see* Kennedy, L J
Ward, T J *see* Schnabel, R D
Ware, W A *see* Magnon, A L
see also Magnon, A L
see also Meurs, K M
Wattrang, E *see* Edfors-Lilja, I
Welzel, K *see* Buitkamp, J
Wende, S, Krempler, A & Brenig, B. Detection of a polymorphic 27 bp insertion/deletion in exon 4 of the canine calcitonin gene-related peptide gene I (*CALCA*), 238
Wernery, U *see* Sasse, J
Whan, V A, Wilson, K J & Moore, S S. Two polymorphic microsatellite markers from novel *Penaeus monodon* ESTs, 143
Wheeler, M B *see* Rahal, P
Wheeler, T T *see* Molenaar, A
Wiener, P *see* Smith, J A
Wiener, P, Maclean, I, Williams, J L & Woolliams, J A. Testing for the presence of previously identified QTL for milk production traits in new populations, 385
Willems, H *see* Reiner, G
Williams, J L *see* Smith, J A
see also Wiener, P
Wilson, A B *see* Noack, K
Wilson, K J *see* Whan, V A
Wimmers, K *see* Trakooljul, N
Wimmers, K, Ponsuksili, S, Hardge, T, Valle-Zarate, A, Mathur, P K & Horst, P. Genetic distinctness of African, Asian and South American local chickens, 159
Windsor, D *see* Smith, J
see also Smith, J
Wise, T H *see* Li, M D
Womack, J E *see* Meurs, K M

see also Rexroad III, C E
Woolliams, J A *see* Wiener, P
Wu, X, Davis, S K, Davis, S L F, Gallagher Jr, D S, Song, Y, Brenneman, R A, Yeh, C-C & Taylor, J F. Assignment of laminin B1 polypeptide (*LAMB1*) and 2,3 bisphosphoglycerate mutase (*BPGM*) to the physical and genetic maps of BTA4, 282

Yamada, T *see* Oishi, M
Yamakuchi, H, Agaba, M, Hirano, T, Hara, K, Todoroki, J, Mizoshita, K, Kubota, C, Tabara, N & Sugimoto, Y. Chediak-Higashi syndrome mutation and genetic testing in Japanese black cattle (Wagyu), 13
Yanai, S *see* Wada, Y
Yang, F *see* Dolf, G
Yang, P C *see* Chen, M Y
Yasue, H *see* Sugai, N
see also Suzuki, K
see also Wada, Y
Yeh, C-C *see* Wu, X
Yerle, M *see* Davoli, R
Yoneda, K *see* Kunieda, T
Yuzbasiyan-Gurkan, V *see* Gray, I S

Zambonelli, P *see* Davoli, R
Zarlenga, D S *see* Sonstegard, T S
Zhao, S *see* Li, K
Zijlstra, C *see* Davoli, R

Animal Genetics, 2000, **31**, 427–428

Keyword index

18S-5.8S-28S ribosomal genes 110

adipose tissue 166
AFLP 117
allele frequency 210, 243
allele-specific PCR 13
arabian horse 1
autosomal recessive disorder 91

bacterial artificial chromosome 8
β-casein 49
beige mouse 13
biodiversity 31, 159
Bos indicus 210
Bos taurus 210
BovA2 277
bovine 210, 262, 277, 306
bovine cDNA library 171
Bovini 178
breed characterization 295
breed relationships 329
breed variation 28
buffalo 277

canine genetics 123
canine linkage map 123
Canis familiaris 310
casein phosphopeptide region 49
cattle 87, 131, 166, 178, 206, 219
CD18 326
Chediak-Higashi syndrome 13, 87
chicken 20, 96, 104, 110, 159, 252
Chinese indigenous pigs 322
chromosome 1 262
chromosome 18 131
chronic interstitial nephritis 91
CHS 13
CHS1 gene 13
CLAD 326
comparative gene mapping 123
comparative mapping 171, 214
conservation 31
Creole cattle 302
CSNK2A2 131

dinucleotide 266
disease resistance 252
divergence times 178
DLA genes and alleles 52
DLA Nomenclature Committee 52
DNA fingerprinting 273
dog chromosome 6 (CFA6) 123
dog 135, 223, 266
dogenic inheritance 223
double-muscling 306
DQA1 200
DQA2 200

equine Celtic breeds 39
European cattle 329
expressed sequence tags 62, 171

fattening 166
FISH 104
follicle-stimulating hormone beta 28
framework map 206

gene duplication 200
gene expression 166
gene mapping 87
gene-density 96
gene-discovery 96
gene-mapping 96
generalised progressive retinal atrophy 135, 223
genetic conversation 29
genetic distance 273, 295, 310
genetic diversity microsatellite 243
genetic diversity 39, 110, 127, 310, 322, 329
genetic introgression 02
genetic map 20
genetic marker 206
genetic resources 159
genetic structure 39
genetics 206
GFD8 306
Golden retrievers 194
growth hormone 210

Holstein Friesian cattle 31
horse genetics 1
horse 1

Iberian pig 117
immune function 186
individual tree 295
integration 20
ITGB2 326

k-casein 277
Korean cattle 49

Labrador retrievers 194
leukocyte numbers 186
library 8
linkage analysis 87
linkage group 20
linkage mapping 171
linkage study 91
linkage 318
lysosomal trafficking regulator 13

macrochromosomes 20
mapping 131, 262
marek's Disease 252
maternal lineage 1
melanocyte-stimulating hormone receptor gene (*MC1R*) 194
Merino sheep 243
MHC genes 219
MHC 252
Mhc*Ovar* 200
microchromosomes 96
microsatellite population structure 310
microsatellite 31, 39, 91, 127, 135, 171, 178, 329
microsatellites 159, 266, 322
minisatellite DNA 273
mitochondrial DNA 1
molecular markers 302
Msp I polymorphism 210
mtDNA 1
muscular hypertrophy 306
myostatin 306

neighbour-joining 295
NOR 110
null allele 200

O. aureus 214
O. niloticus 214

PCR 104
PCR-RFLP 13, 318
PDE6A 135
phenotyping 219
phylogeny 178
physical map 20
physical mapping 318
pig breed differentiation 273
pigs 186, 318
polymorphism 171, 210, 252, 266
premature stop codon 194
pseudogene 131
pyrosequencing 326

QTLs 186

radiation hybrids 262
rDNA 110
RDS/Peripherin 223
repetitive DNA 104
retinitis pigmentosa 135, 223
retroposon 131
rOM1 223
rules for acceptance 52

sequence analysis 62
sequence based nomenclature 52
sequence-sampling 96
sex diagnosis 104
short interspersed elements (SINEs) 277
short tandem repeats 295
single cell detection 104
SNP 318
SSC7 318
SSCP 135, 223
Stress 186
STS 318

© 2000 International Society for Animal Genetics

swine 8, 28
synteny 131

taurine cattle 127
tilapia 214
transfection 219
trinucleotide 266
turkey 62
type II markers 214

variant 49

Wagyu cattle 13

Y chromosome polymorphism 302
Y-chromosome 127

Zebu cattle 127